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An Improved Optimization Strategy for Seed Liquid Preparation and Fermentation Process

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ABSTRACT

Seed liquid preparation and fermentation process are two key production stages in the production process of *Bacillus licheniformis*, which are commonly used in microbial agents. The study of process optimization is of practical significance to improve the product quality of pharmaceutical enterprises. In the process of seed liquid preparation and fermentation of *Bacillus licheniformis*, there are many variables and complexities, and there are many dynamic and nonlinear links, and the process is difficult to be accurately described by the mechanism model. Its dynamic characteristics make it difficult to keep the control variables at a specific level, resulting in it being difficult to ensure the accuracy of the model and the optimization performance needs to be improved. In order to solve the above problems, firstly, the modeling method of BP neural network is used to select the variables which play an important role in the results, a two-stage mapping model based on LSSVM is established and the optimization model of differential evolution algorithm is proposed to solve the problem. Targeting the problem of multi-stage model integration, rolling optimization is applied to dynamically adjust the decision variables such as fermentation temperature and rotation, so as to achieve the goal of increasing the number of living bacteria and reducing the loss of raw materials at the same time. The experimental results based on the actual production data show that the method can optimize the fermentation process accurately and effectively.

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1. Introduction

As a feed additive, antibiotics play an active role in animal and poultry epidemic prevention. However, in the past 10 years, there have been many opinions in the foreign feed industry and breeding industry against the use of antibiotics for feed addition^[1]. Therefore, experts and scholars at home and abroad are paying more and more attention to the research on the development of microecological preparations for livestock and poultry breeding^[2], which also promotes the rapid development of this industry. The main domestic micro-ecological additives are some spores and lactic acid bacteria^[3], but the production cost has been high for a long time. To solve this problem, the optimal control of the fermentation process of *B. licheniformis* is beneficial to increase the yield, reduce manufacturing cost. The fermentation process is an important process in the pharmaceutical production process.

The live bacteria of *Bacillus licheniformis*, as a finished product in the fermentation production process, need to be prepared through a two-step process of seed liquid preparation and fermentation. First, the production seed liquid preparation process is carried out, mainly to complete the preparation of the seed liquid. The lyophilized powder in the lyophilized tube is transferred to the sterilized broth medium, and the inoculated medium is sent to a constant temperature oscillator for cultivation. After the completion of the

culture, the smear microscopy is performed under aseptic conditions. Observe the number of strains and record, transfer the qualified seed production liquid into the inoculation bottle, and mark it; then enter the fermentation process, weigh the material into the fermenter according to the ratio, and then sterilize it by air separation. The tank can be sterilized, inoculated, cultured, sampled and microscopically examined, placed in a can, boiled in a pot, etc., and the strain is cultured to obtain live bacteria.

The process flow is shown in the following figure:

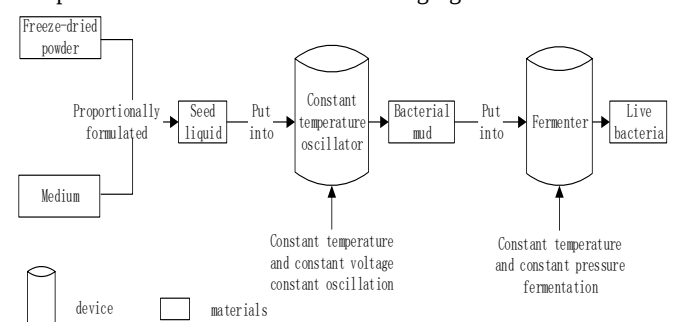


Figure 1 Process flow chart of fermentation process

When the detection of the number of viable bacteria and other indicators meets the requirements, the fermentation production process is completed. The whole preparation process is reflected in the macroscopic characteristics, that is, the parameters such as

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temperature and time involved in each step are required to reach a level suitable for fermentation.

Therefore, aiming at the current production status of *B. licheniformis* seed liquid preparation and fermentation process, it is of great practical significance to control and optimize the fermentation production process with the goal of increasing the number of live bacteria and reducing the loss of raw materials^[4]. In order to rapidly increase the fermentation productivity and fermentation level, the traditional fermentation process is more focused on the screening and transformation of the strain itself^[5]; with the development of biological science and technology, the research in the field of genetic engineering and metabolic engineering has made great progress. With the development, the use of genetic recombination and induction techniques can achieve high-yield strains^[6], but this method is difficult to optimize the product quality and raw material cost of the fermentation process. In this paper, the modelling of fermentation process is used to optimize the fermentation process to achieve the highest product quality, maximum productivity and lowest cost. The optimal control of microbial fermentation process can be divided into process model and optimization control strategy^[7]. The modeling of the fermentation process includes:

(1) Mechanism analysis of the fermentation process, that is, based on the biological equation and the gene scale level, and the model parameters are determined according to the regression method. Zhang Cuiping, Li Huijuan et al^{[8][9]} carried out the optimization of fermentation process from the aspects of gene and cell characteristics, and put forward new insights on the process and essence of the model, established the mechanism model of the strain, and further obtained the limitation of fermentation engineering condition. However, compared with the complexity of the actual fermentation process, the mechanism modeling only contains state variables such as biomass and products, and cannot fully express the microbial fermentation process, and its accuracy and universality have great limitations;

(2) black box Modeling, a fermentation process model based on least squares regression identification, has a high adaptability^[10]. Modeling the process with least squares regression combines the advantages of the classical control method, is technically simple and easy to operate, and has diagnostic capabilities. In addition, some nonlinear functions are also widely used in process modeling, mainly artificial neural network (ANN) and support vector machine technology (SVM); (3) modeling of fermentation process based on the method, online correction ability for ANN A strong, suitable feature for dealing with multivariate nonlinear problems establishes a more accurate model. Wang Jian et al^[11] used the standard neural network BP algorithm to simulate the fermentation of acid in the fermentation process of L-tryptophan, but required a large amount of experimental data feedback, and the prediction error was high. SVM does not have too high dependence on the sample. Compared with the ANN method, the SVM method not only has a relatively low relative error in the prediction of the fermentation process, but also effectively solves the problems of nonlinearity and local minimum^{[12][13][14]}. SVM-based modeling of the fermentation process of microbial strains ensures the accuracy of modeling and saves a lot of time.

At present, in the optimization control strategy, the classical optimization control method based on linear approximation is widely used in the optimization control of early fermentation process^[15]. The maximum value principle and the iterative method

are used in the state space description of the fermentation process to achieve the optimal implementation effect of the fermentation. The maximum value principle method is suitable for more complicated fermentation process control objects, but the maximum value principle can only be obtained by open-loop control. When the calculation amount of the fermentation process is large, only the optimization curve can be developed for a few processes, and neglected. The interference of environmental factors on the system; in the 1960s, with the introduction of differential geometry methods, the study of nonlinear system theory entered a new stage^[16]. Relevant researchers have established a nonlinear fermentation space model. The controller designed by the differential method has obtained excellent control effects in the fermentation process and effectively improved the dynamics of the fermentation control process. However, the mathematical geometry method itself has higher requirements on the accuracy of the system model. Combined with the complexity of the fermentation process, this method is not conducive to the stability of the fermentation control system. In recent years, the use of computer science technology combined with artificial intelligence theory to optimize the fermentation process has become In recent years, the research hotspot of fermentation process, the application of artificial intelligence technology can break through many complex system problems^[17]. Niu Dapeng et al^[18] used the intelligent method to optimize the fermentation process in the literature based on the improved multi-objective differential evolution algorithm for the optimization of norozyme fermentation process, and then applied the differential evolution algorithm to solve the multi-objective optimization model. Numerical simulation experiments results show that this method achieves excellent results and the stability of the system is also improved.

In summary, this paper adopts a two-stage reverse modeling strategy based on DE-LSSVM to establish a model for the fermentation process of *Bacillus licheniformis*: firstly, the BP neural network method is used to filter the variables, then the multi-stage mapping model is established based on LSSVM, and then the difference is applied. The evolutionary algorithm solves the optimization model. Finally, the rolling optimization is used to dynamically adjust the decision variables such as fermentation temperature and number of revolutions to achieve the goal of increasing the number of viable bacteria while reducing the loss of raw materials.

2. Variable Filtering Based on BP Neural Network

2.1 Data preprocessing

The data sample used in this paper is from the real production data of a pharmaceutical factory in Liaoning Province. The production process of seed liquid preparation and fermentation is selected. 50 batch production records are selected for key process parameters, including nutrient broth medium dosage and culture time. , culture temperature and number of revolutions and other data.

Firstly, manual processing is carried out. The production data of the pharmaceutical factory contains individual and singular data. If these singular data are only normalized, the improvement degree is very limited. Therefore, according to the actual situation and prior knowledge of the pharmaceutical factory, Manual processing to rationalize the data; then normalized^[19], the expression is as follows:

$$y(i) = \frac{u(i) - u_{min}}{u_{max} - u_{min}} \quad (1)$$

Where $u(i)$ is the data before the normalization process, u_{max} , u_{min} are the maximum and minimum values of the data $u(i)$, respectively, and $y(i)$ is the normalized data^[20]. After the above data preprocessing, the rationality of the obtained data is improved, which can be used for the next step of screening variables and establishing a system model.

2.2 Neural Network Variables Screening Using BP Network

Table 1 Sorting of MIV values of related factors in seed preparation process

variable name	MIV value	sort
Number of live bacteria	4.42	1
Bacterial weight	3.79	2
Number of strains	3.49	3
Culture temperature	2.87	4
Air flow	2.84	5
PH value	2.72	6
Growth time	2.64	7
Purified water pH	0.24	8
Purified water flow	1.01	9

Table 2 Sorting of MIV values of factors related to fermentation process

variable name	MIV value	sort
Medium dosage	3.70	1
Freeze-dried powder	3.16	2
Culture temperature	1.91	3
Training time	2.61	4
Number of revolutions	0.74	5

MIV (Mean Impact value) is an index used to determine the influence of input neurons on the output neurons. The positive and negative signs represent the relevant directions, and the absolute value represents the relative importance of the effects^[21]. In this paper, the BP neural network is used to apply the average impact value MIV to filter the variables to find the inputs that have a greater impact on the results. The specific calculation process is as follows:

(1) After the BP neural network training is stopped, each of the independent variables in the training

sample S is added/multiplied by 10% on the basis of its original value to form two new training samples S1 and S2;

(2) Using S1 and S2 as simulation samples respectively, and using the established network for simulation, two simulation results Q1 and Q2 are obtained;

(3) Calculate the difference between Q1 and Q2 as the change value of the influence on the output after changing the independent variable;

(4) The MIV is averaged according to the number of observations to obtain the corresponding variable of the independent variable, that is, the MIV outputted by the network, and the MIV values of the respective independent variables are sequentially calculated according to the above steps;

(5) Sorting the MIV according to the size of its absolute value, that is, obtaining the ranking table of the relative importance of the respective variables on the network output, and judging the influence degree of the input characteristics on the network results according to the table, so as to realize the utilization of BP Neural network screening of variables.

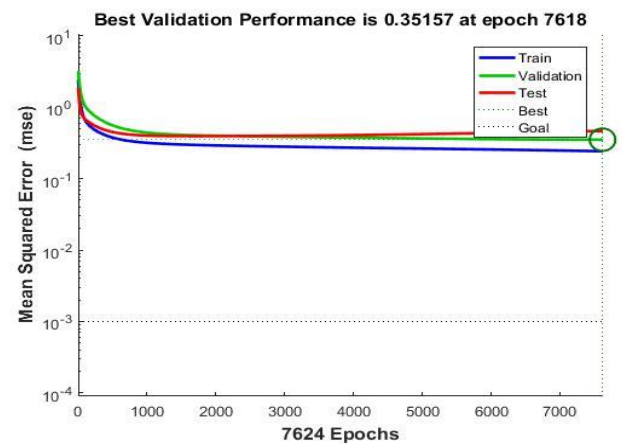


Figure 2. Neural network model MATLAB simulation results for the fermentation phase

Using the above method, through MATLAB simulation, the results were obtained: BP neural network model of seed liquid preparation and fermentation process, and training charts and MIV value ranking tables of related factors were established. The BP neural network training diagram is shown in Figure 2 and Figure 3. The order of magnitude of the correlation factor MIV values is shown in Table 1 and Table 2.

Through the simulation modeling of BP neural network, the weight of each model and each variable can be obtained. According to the feedback result of the model, the results are as follows:

(1) In the fermentation stage, the input variables are the viable cell count n_2 , the culture temperature T_2 , the tank pressure P_1 , the air flow rate s , and the growth time t_2 , and the output variables are the slime weight W_3 , the pH value e_1 , and the number of strains n_1 .

(2) In the preparation stage of the seed liquid, the input variables are the slime weight W_3 , the PH value e_1 , the number of strains n_1 , and the output variables are the medium dosage W_1 , the lyophilized powder dosage W_2 , the time t_1 , and the temperature T_1 .

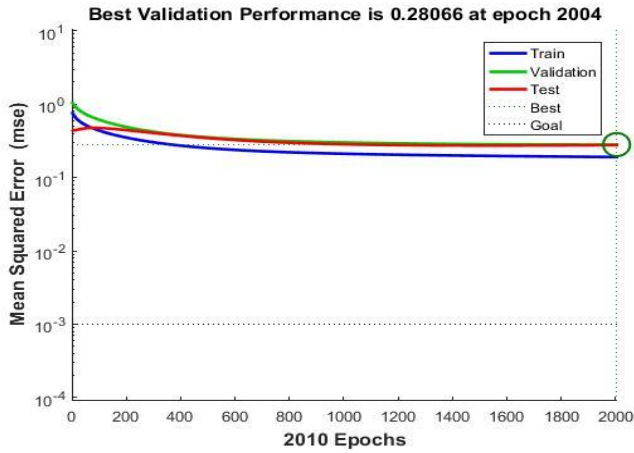


Figure 3. Neural network model MATLAB simulation results in seed preparation stage

3. LSSVM multi-stage inverse model modeling

3.1 Introduction of Least Squares Support Vector Machine (LSSVM)

The Least Squares Support Vector Machine is a new support vector machine method proposed by Suykens, Vandewalle et al. based on Vapnik statistical learning theory. It has a rigorous mathematical foundation and is based on structural risk minimization criteria. It still has good statistical laws and good generalization ability in the case of small samples. LSSVM introduces the least squares linear system into the support vector machine as the loss function, instead of using the quadratic programming method to solve the classification and function estimation problems in the traditional support vector machine. LSSVM is still a kernel function-based machine learning. It extracts features from the original space according to the Mercer condition, and maps the samples in the original space to a vector in the high-dimensional feature space to solve the linear indivisibility problem in the original space. An extension of the traditional support vector machine; a form of support vector machine under the quadratic loss function. Since only linear equations are solved, LSSVM has the advantages of simple solution and fast convergence, and has been widely used in function estimation and approximation [22].

3.2 Function Estimation Using Least Squares Support Vector Machine

For a given set of training samples $D = \{(x_k, y_k) / k=1, 2, \dots, N\}$, where N is the number of samples, $x_k \in \mathbb{R}^n$ is the input data, $y_k \in \mathbb{R}^n$ Output data, nonlinear feature map $\mathbb{R}^n \rightarrow H$ (H is the feature space), define the function $y(x)$ based on training set D to Close to the unknown function $g(x)$.

$$y(x) = w^T \phi(x) + b \quad (2)$$

Where w is the weight vector in the feature space and $b \in \mathbb{R}$ is the

offset. Introduce a structural risk function to transform the regression problem into the following quadratic optimization problem.

$$\min J = \min \left(\frac{1}{2} w^T w + \gamma \frac{1}{2} \sum_{i=1}^n e_k^2 \right) \quad (3)$$

The constraint is:

$$y_k = w^T \phi(x_k) + b + e_k, \quad k=1, \dots, n. \quad (4)$$

Where $\phi(\cdot)$ is a nonlinear transformation function that transforms the input space into a high-dimensional space, e is a slack term, and γ is an error penalty.

The corresponding Lagrange function is

$$L(w, b, e, \alpha) = J(w, e) - \sum_{k=1}^N \alpha_k \{w^T \phi(x_k) + b + e_k - y_k\} \quad (5)$$

Where $\alpha_k \in \mathbb{R}$ is a Lagrange multiplier according to KKT conditions

$$\frac{\partial L}{\partial w} = 0 \rightarrow w = \sum_{k=1}^N \alpha_k \phi(x_k) \quad (6)$$

$$\frac{\partial L}{\partial b} = 0 \rightarrow \sum_{k=1}^N \alpha_k = 0 \quad (7)$$

$$\frac{\partial L}{\partial e_k} = 0 \rightarrow \alpha_k = \gamma e_k \quad (8)$$

$$\frac{\partial L}{\partial \alpha_k} = 0 \rightarrow w^T \phi(x_k) + b + e_k - y_k = 0 \quad (9)$$

For $k = 1, \dots, n$, w and e are eliminated in the above equation, resulting in a linear system of the form:

$$\begin{bmatrix} 0 & \vec{1}^T \\ \vec{1} & Z Z^T + \gamma^{-1} I \end{bmatrix} \begin{bmatrix} b \\ \vec{\alpha} \end{bmatrix} = \begin{bmatrix} 0 \\ Y \end{bmatrix} \quad (10)$$

Where $Z = [\phi(x_1)^T y_1, \dots, \phi(x_N)^T y_N]$, $Y = [y_1, \dots, y_N]$, $\vec{1} = [1, \dots, 1]$, $e = [e_1, \dots, e_n]$, $\vec{\alpha} = [\alpha_1, \dots, \alpha_n]$, is the identity matrix. Depend on the Mercer condition, the following equation is established:

According to the Mercer condition, the following equation is established.

$$\Omega_{kl} = y_k y_l \phi(x_k)^T \phi(x_l) = y_k y_l K(x_k, x_l) \quad (11)$$

So the linear equations can be rewritten as:

$$\begin{bmatrix} 0 & \vec{1}^T \\ \vec{1} & \Omega + \gamma^{-1} I \end{bmatrix} \begin{bmatrix} b \\ \vec{\alpha} \end{bmatrix} = \begin{bmatrix} 0 \\ Y \end{bmatrix} \quad (12)$$

Nonlinear regression function is

$$y_k = \sum_{j=1}^N \alpha_j K(x_j, x_k) + b \quad (13)$$

Where a and b are equations solutions.

In this way, although the sample data is mapped to a feature space with high or even infinite dimensions through a nonlinear function, it is not necessary to explicitly calculate the nonlinear function when calculating the regression estimation function, and only the kernel function is calculated, thereby avoiding high Dimension disaster caused by dimension feature space.

3.3 Multi-stage inverse model modeling of fermentation process based on LSSVM

Firstly, the inverse model of the fermentation stage is established. In this stage, the final product quality index of the live

bacterial production process is taken as the input variable, and the corresponding control variable and the output variable from the previous stage are used as the output variables of this stage. The inverse model is based on LSSVM. Modeling. Through the analysis of the process and input and output data, and the screening of BP neural network, five key input variables at this stage are determined, namely: the number of viable bacteria n_2 , tank pressure P_1 , culture temperature T_2 , air flow rate s , growth time t_2 ; three key output variables, followed by: sludge weight W_3 , pH value e_1 , number of strains n_1 . Therefore, it can be expressed as the following function expression:

$$W_3=f_1(t_2, P_1, t_3, s, T_2) \quad (14)$$

Where f_1 is a nonlinear regression estimation function. E_1 and N_1 are regression functions as shown in the following function expression.

$$E_1=f_2(t_2, P_1, t_3, s, T_2) \quad (15)$$

$$N_1=f_3(t_2, P_1, t_3, s, T_2) \quad (16)$$

Radial basis function (RBF) is used in LSSVM modeling.

$$K(X, X_i)=exp\left\{-\frac{|X-X_i|^2}{\sigma^2}\right\} \quad (17)$$

As a kernel function of the SVM, the RBF kernel function has good performance under the assumption of general smoothness. In order to increase the reliability of the experimental results, this paper uses cross-validation methods to obtain optimized parameters [23].

The sample set S composed of the data pre-processed and normalized samples is divided into three parts, which are respectively recorded as sample sets S_1 , S_2 , and S_3 ; S_1 is a training set, which is composed of 30 sets of samples, used for training and modeling S_2 . S_3 is a test set, each consisting of 10 sets of samples.

After training, a nonlinear mathematical model of the slime weight W_5 , the pH value e_3 , the number of strains n_3 , and the drying temperature t_4 can be obtained.

Based on the same method, an inverse model of the seed liquid preparation stage can be established. The input variables are the sludge weight W_3 , the pH value e_1 , the number of strains n_1 , and the output variables are the medium dosage W_1 , the lyophilized powder dosage W_2 , the number of revolutions N , Time t_1 , temperature T_1 .

$$W_1=f_4(W_3, e_1, n_1) \quad (18)$$

$$W_2=f_5(W_3, e_1, n_1) \quad (19)$$

$$t_1=f_7(W_3, e_1, n_1) \quad (20)$$

$$T_1=f_8(W_3, e_1, n_1) \quad (21)$$

Thus, we established a two-stage LSSVM inverse model for the preparation and fermentation of *Bacillus licheniformis* seed solution. However, the parameter problem of the model will affect the accuracy of the model, so the next step of this paper will further optimize the model parameters of LSSVM.

4. DE-based LS-SVM parameter optimization

In the modeling of the preparation and fermentation process of *Bacillus licheniformis* seed solution using LSSVM, the parameter selection of LSSVM has an important influence on the performance of the constructed model. In this paper, the differential evolution algorithm is used to optimize the parameters of LSSVM to improve the performance of the two-stage LSSVM model.

The Different Evolution (DE) is a population search-based evolutionary algorithm proposed by Store and Price in 1995. It

extracts differential information from the current population to guide the next search. The DE algorithm includes three operations: mutation, intersection and selection. The basic steps are: firstly extract the search step and direction information from the population, and then add random difference and crossover operations to improve the diversity of the current population. The current population obtains a temporary population through mutation and crossover, and then the two populations are subjected to a one-to-one comparison selection operation based on the magnitude of the objective function value, thereby generating a new generation population [24]. The population is continuously evolved as described above until the termination condition is met.

For the LSSVM with RBF as the kernel function, the penalty parameter C and the kernel parameter a are the main factors affecting the classification performance of LSSVM. Because the DE algorithm has better global search ability and strong robustness, this paper uses differential evolution algorithm to optimize the parameters of LSSVM.

The steps of LSSVM parameter optimization based on differential evolution algorithm are as follows [25]:

- (1) Normalize the sample data and divide it into two parts: test set and training set. The DE algorithm initializes the operation, and sets the upper and lower limits of the population size N , the maximum evolution algebra gm , the scaling factor k , the crossover probability CR , the LSSVM penalty parameter C and the kernel parameter σ , and generates a random parameter (C, σ) ;
- (2) Using the currently generated (C, σ) as a parameter of LSSVM, using LSSVM to train and test the sample data to obtain training results;
- (3) Comparing the obtained classification result with the actual value, calculating the objective function value, judging whether the stop condition $g=gm$ is satisfied, and if satisfied, outputting the optimal parameter (C, σ) , if not satisfied, proceeding to the next step;
- (4) Perform mutation, crossover and selection operations on the individual, generate new parameters (C, σ) , and then transfer to 2).

Among them, the three operating procedures of the DE algorithm are described as follows:

- (1) Variation: randomly select 4 different individuals x_i^g from the current g generation population, and use the formula (24) to perform the mutation operation to obtain the $g+1$ variant individual v_i^{g+1} ;

$$v_i^{g+1}=x_{best}^{g+1}+k[(x_{i1}^{g+1}-x_{i2}^{g+1})+(x_{i3}^{g+1}-x_{i4}^{g+1})] \quad (22)$$

- (2) Crossover: cross-operate the $g+1$ variant individual v_i^{g+1} according to formula (25) to obtain $g+1$ experimental individual y_i^{g+1}

$$y_i^{g+1}=\begin{cases} v_{ij}^{g+1}, & \text{rand}(j) \leq CR \\ x_{ij}^g, & \text{rand}(j) > CR \end{cases} \quad (23)$$

- (3) Selection: Selecting the $g+1$ generation experimental individual y_i^{g+1} according to formula (26), and obtaining $g+1$ individual x_i^{g+1} ,

$$x_i^{g+1}=\begin{cases} y_i^{g+1}, & f(y_i^{g+1}) < f(x_i^g) \\ x_i^g, & f(y_i^{g+1}) \geq f(x_i^g) \end{cases} \quad (24)$$

In the process of optimizing the parameters of the DE algorithm, two algorithm stopping criteria are set: one is to set the maximum iteration number g_{max} of the algorithm to prevent the algorithm from

falling into an infinite loop to ensure that the algorithm can output the result within the specified time; the second is that if the algorithm obtains the solution Continuous iteration g_N times without improvement then stop. If any of the above stopping criteria is met, the algorithm stops running and outputs the result. The optimization of the kernel parameters of the LSSVM by the DE algorithm can improve the compensation accuracy of the LSSVM for the output of the mechanism model [26].

The optimal parameters (C , σ) of the LSSVM are obtained, and the sample data is trained and tested using the LSSVM.

5. Simulation and analysis

In order to test the validity and accuracy of the two-stage inverse model based on LS-SVM, a series of simulation experiments were carried out to verify the performance of the model for the fermentation process of *Bacillus licheniformis*.

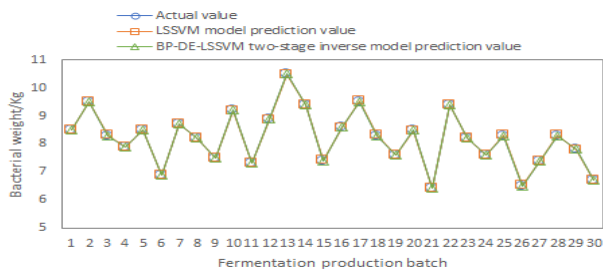


Figure 4 Prediction value of Bacterial weight

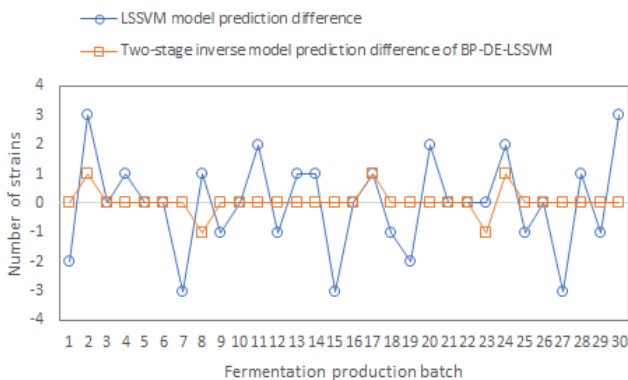


Figure 5 Prediction difference of Bacterial weight

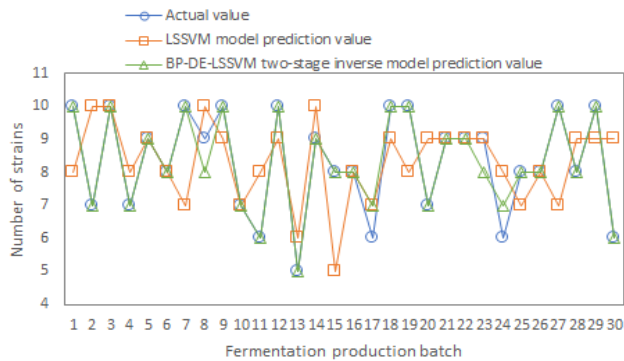


Figure 6 Prediction value of the number of strains

The simulation data of 30 fermentation batch data in the production process of the factory was taken as the decision object data. Each set of data includes: slime weight, pH value, and number of strains. For the three experimental indicators, the comparison curve

between the predicted value and the actual value of the LSSVM model and the BP-DE-LSSVM two-stage inverse model and the predicted deviation comparison curve are shown in Figures 4, 5, 6, 7, 8 and 9.

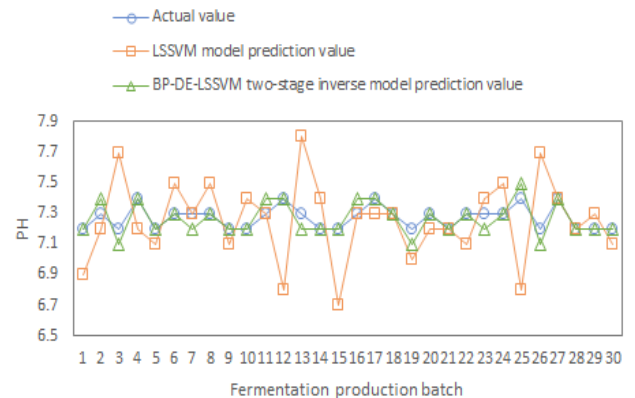


Figure 7 Prediction difference of the number of strains

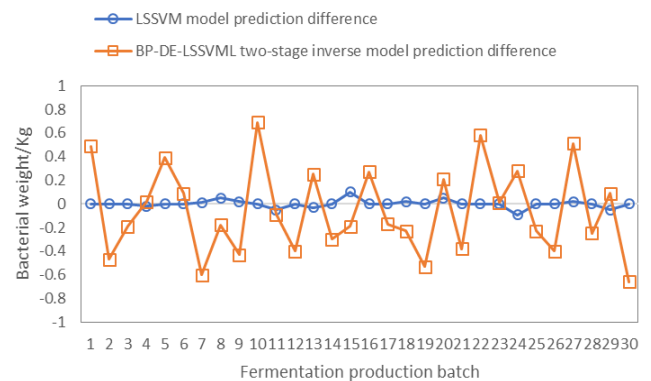


Figure 8 Prediction value of PH values

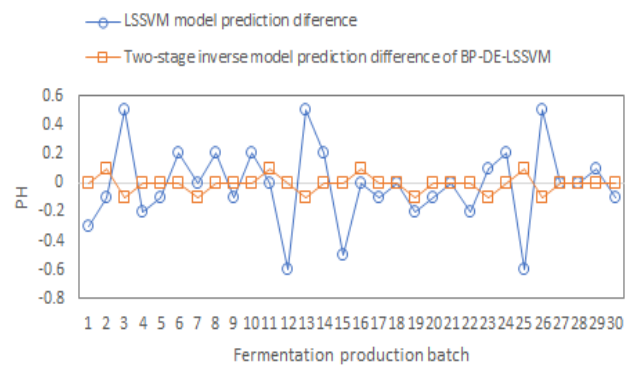


Figure 9 Prediction difference of PH values

It can be seen from the above figure that the prediction results of the two-stage reverse model using BP-DE-LSSVM can accurately track the actual temperature value, and at the same time, from the comparison results of the prediction error curve, it can be seen that the prediction deviation of the number of live bacteria errors is close to one The straight line (that is, the error is close to 0); most of the prediction deviation of the weight of the slime is less than 0.1Kg; the prediction deviation of the error of the PH value is less than 0.2.

From the above experimental results, it can be seen that the two-stage reverse model based on BP-DE-LSSVM can significantly improve the prediction accuracy of the prediction model, verifying

the effectiveness and accuracy of the hybrid modeling method in the optimization of the *Bacillus licheniformis* fermentation production process.

6. Conclusion

Aiming at the optimization modeling problem of *Bacillus licheniformis* fermentation process with complex, dynamic and nonlinear characteristic processes, this paper proposes a two-stage reverse modeling method based on BP-DE-LSSVM. Firstly, the MIV-BP neural network data method is used to screen the variables and data with large impact value. Then, the two-stage inverse model is established based on LSSVM. Finally, the model kernel parameters are optimized based on the DE algorithm to achieve the purpose of improving the accuracy of the model. The numerical experiments on the performance of the model show that the modeling strategy effectively improves the performance of the model and shows significant advantages in both effectiveness and precision.

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